

SEQUENCE LISTING

<110> Elliott, Steven G.
Rogers, Norma
Busse, Leigh Anne

<120> G-Protein Coupled Receptor Molecules and Uses Thereof

<130> 02-076

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<150> 60/269,040

<151> 2001-02-14

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 1038

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1038)

<400> 1

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Met	Tyr	Asn	Gly	Ser	Cys	Cys	Arg	Ile	Glu	Gly	Asp	Thr	Ile	Ser	Gln	
1				5				10					15			

gtg	atg	ccg	ccg	ctg	ctc	att	gtg	gcc	ttt	gtg	ctg	ggc	gca	cta	ggc	96
Val	Met	Pro	Pro	Leu	Leu	Ile	Val	Ala	Phe	Val	Leu	Gly	Ala	Leu	Gly	
			20					25					30			

aat	ggg	gtc	gcc	ctg	tgt	ggc	ttc	tgc	ttc	cac	atg	aag	acc	tgg	aag	144
Asn	Gly	Val	Ala	Leu	Cys	Gly	Phe	Cys	Phe	His	Met	Lys	Thr	Trp	Lys	
		35					40					45				

ccc	agc	act	gtt	tac	ctt	ttc	aat	ttg	gcc	gtg	gct	gat	ttc	ctc	ctt	192
Pro	Ser	Thr	Val	Tyr	Leu	Phe	Asn	Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu	
	50					55					60					

atg	atc	tgc	ctg	cct	ttt	cgg	aca	gac	tat	tac	ctc	aga	cgt	aga	cac	240
Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg	Arg	Arg	His	
65				70					75					80		

tgg	gct	ttt	ggg	gac	att	ccc	tgc	cga	gtg	ggg	ctc	ttc	acg	ttg	gcc	288
Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe	Thr	Leu	Ala	
			85					90						95		

atg	aac	agg	gcc	ggg	agc	atc	gtg	ttc	ctt	acg	gtg	gtg	gct	gcg	gac	336
Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val	Ala	Ala	Asp	
			100					105					110			

caa tgg gat ccc cac att gtt gag tgg cac
 Gln Trp Asp Pro His Ile Val Glu Trp His
 340 345

1038

<210> 2
 <211> 346
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
 35 40 45
 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
 50 55 60
 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
 65 70 75 80
 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
 85 90 95
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
 100 105 110
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
 115 120 125
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 130 135 140
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
 145 150 155 160
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 165 170 175
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
 180 185 190
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
 195 200 205
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
 210 215 220
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
 225 230 235 240
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val

204733 09294007

	245		250		255
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met					
	260		265		270
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe					
	275		280		285
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His					
	290		295		300
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg					
	305		310		315
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly					
		325	330		335
Gln Trp Asp Pro His Ile Val Glu Trp His					
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<210> 3
 <211> 3251
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (350)..(1402)

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 cgcttgacc ccagagcctg acccagctgc aggttcaac tctgtagggg acgtgcagct 180
 cgtgatccaa gcctaggaga aaggacttgc tgccggcttt catttcctgg ctgaagtttc 240
 tctcgtgggt gcagcgctg catcccaggg tgatgaggtt aggggccag ctgctagagg 300
 agccctagtg ttcggatagg cagctgtgcc tctgtgccgg ccaccttg atg cca gtc 358
 Met Pro Val
 1

ctc tct cca act gct atg gac aac ggg tgc tgc tgt ctc atc gag ggg	406
Leu Ser Pro Thr Ala Met Asp Asn Gly Ser Cys Cys Leu Ile Glu Gly	
5 10 15	

gag ccc atc tcc cag gtg atg cct cct cta ctc atc ctg gtc ttc gtg	454
Glu Pro Ile Ser Gln Val Met Pro Pro Leu Leu Ile Leu Val Phe Val	
20 25 30 35	

ctt ggc gcc ctg ggc aac ggc ata gcc ctg tgc ggc ttc tgc ttt cac	502
Leu Gly Ala Leu Gly Asn Gly Ile Ala Leu Cys Gly Phe Cys Phe His	
40 45 50	

Tyr	Leu	Asn	Ser	Met	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	
				280					285					290		
tcg	ctc	ccc	aaa	ttc	tac	gcc	aag	ctc	aca	atc	tgc	agc	ctg	aag	ccc	1270
Ser	Leu	Pro	Lys	Phe	Tyr	Ala	Lys	Leu	Thr	Ile	Cys	Ser	Leu	Lys	Pro	
			295					300					305			
aaa	cgc	cca	gga	cgc	acg	aag	acg	cgg	agg	tca	gaa	gag	atg	cca	att	1318
Lys	Arg	Pro	Gly	Arg	Thr	Lys	Thr	Arg	Arg	Ser	Glu	Glu	Met	Pro	Ile	
		310					315					320				
tcg	aac	ctc	tgc	agt	aag	agc	tcc	atc	gat	ggg	gca	aat	cgt	tcc	cag	1366
Ser	Asn	Leu	Cys	Ser	Lys	Ser	Ser	Ile	Asp	Gly	Ala	Asn	Arg	Ser	Gln	
	325					330				335						
agg	cca	tct	gac	ggg	cag	tgg	gat	ctc	caa	gtg	tgt	tgaatgccat				1412
Arg	Pro	Ser	Asp	Gly	Gln	Trp	Asp	Leu	Gln	Val	Cys					
340					345				350							
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aatcctccct	tctcaagtct	ttgtttaatc	cacagtatgt	tgtcccaccc	tgtccagcat											2252
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tagccaactt	ttgggagaaa	gcaaagcact	agaggtggca	gcaacagttt	agctcaatgt											2432
cctttcgtca	gtgtctagac	ttctgggtcag	ccatccgggt	ctcctattgg	gggcctccct											2492
caagcacata	tgttctccca	aatactaccc	agaattctca	cagctagggtg	attctgtgaa											2552

agtccaggct gccctgtcc tggagaagga gaaatagaat ccgtgttaac cttagtccca 2612
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 ccagggaagg gaccttgaca tttatgtcta aagacataaa ttagatgctc ctcaagggtg 2732
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 tccctgagac ccacgtggta ggagaacacc aaatcccaaa ggtggttctg tcctccacct 2912
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 ttaatgcaat aaaaatttta ttggctacac ggtcaagttt gaatcttagt ttaaattgctt 3032
 attagacatg tgctcgtagg gaagacttta ttttaaccca ctcaagtttg atgttcagca 3092
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 tgagaaatct gttgttccca ggtctgcccg gaagaagacc atgtgcgtgt agtagttgat 3212
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<210> 4

<211> 351

<212> PRT

<213> Mus musculus

<400> 4

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			20					25						30	
Val	Phe	Val	Leu	Gly	Ala	Leu	Gly	Asn	Gly	Ile	Ala	Leu	Cys	Gly	Phe
		35					40					45			
Cys	Phe	His	Met	Lys	Thr	Trp	Lys	Ser	Ser	Thr	Ile	Tyr	Leu	Phe	Asn
	50					55					60				
Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu	Met	Ile	Cys	Leu	Pro	Leu	Arg	Thr
65					70					75					80
Asp	Tyr	Tyr	Leu	Arg	Arg	Arg	His	Trp	Ile	Phe	Gly	Asp	Ile	Ala	Cys
				85					90					95	
Arg	Leu	Val	Leu	Phe	Lys	Leu	Ala	Met	Asn	Arg	Ala	Gly	Ser	Ile	Val
			100					105					110		
Phe	Leu	Thr	Val	Val	Ala	Val	Asp	Arg	Tyr	Phe	Lys	Val	Val	His	Pro
		115					120					125			
His	His	Met	Val	Asn	Ala	Ile	Ser	Asn	Arg	Thr	Ala	Ala	Ala	Thr	Ala
	130					135								140	

Cys Val Leu Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Met
 145 150 155 160
 Glu Ser His Leu Cys Val Gln Gly Thr Leu Ser Ser Cys Glu Ser Phe
 165 170 175
 Ile Met Glu Ser Ala Asn Gly Trp His Asp Val Met Phe Gln Leu Glu
 180 185 190
 Phe Phe Leu Pro Leu Thr Ile Ile Leu Phe Cys Ser Val Asn Val Val
 195 200 205
 Trp Ser Leu Arg Arg Arg Gln Gln Leu Thr Arg Gln Ala Arg Met Arg
 210 215 220
 Arg Ala Thr Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr Cys
 225 230 235 240
 Tyr Leu Pro Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro
 245 250 255
 Thr Ser Ala Cys Asp Pro Ser Val His Thr Ala Leu His Val Thr Leu
 260 265 270
 Ser Phe Thr Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe
 275 280 285
 Ser Ser Pro Ser Leu Pro Lys Phe Tyr Ala Lys Leu Thr Ile Cys Ser
 290 295 300
 Leu Lys Pro Lys Arg Pro Gly Arg Thr Lys Thr Arg Arg Ser Glu Glu
 305 310 315 320
 Met Pro Ile Ser Asn Leu Cys Ser Lys Ser Ser Ile Asp Gly Ala Asn
 325 330 335
 Arg Ser Gln Arg Pro Ser Asp Gly Gln Trp Asp Leu Gln Val Cys
 340 345 350

<210> 5
 <211> 1668
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (365)..(1417)

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 agacccccaa gctgcagcct ggcaatgtac gcttttggaa aactgctctc gcctcagagc 180

gtt tgg agc ctg aga cag agg caa cag ctg acc aga cag gct cgg atg 1033
Val Trp Ser Leu Arg Gln Arg Gln Gln Leu Thr Arg Gln Ala Arg Met
210 215 220

agg agg gcc acc cgg ttc atc atg gtg gtg gct tcc gtg ttc atc acg 1081
Arg Arg Ala Thr Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr
225 230 235

tgt tac ctg ccc agc gtg ttg gcg agg ctc tac ttc ctc tgg acg gtg 1129
Cys Tyr Leu Pro Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val
240 245 250 255

ccc tcc agt gct tgt gac ccc tct gtc cac ata gct ctc cat gtc acc 1177
Pro Ser Ser Ala Cys Asp Pro Ser Val His Ile Ala Leu His Val Thr
260 265 270

ctg agt ctc acc tac ctg aac agc atg ctg gac cct ctt gtg tac tac 1225
Leu Ser Leu Thr Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr
275 280 285

ttt tca agc ccc tcg ttc ccc aaa ttc tac gcc aag ctc aaa atc cgc 1273
Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Ala Lys Leu Lys Ile Arg
290 295 300

agc ttg aaa ccc aga cgc cca gga cgc tcg cag gca cgg agg tcg gaa 1321
Ser Leu Lys Pro Arg Arg Pro Gly Arg Ser Gln Ala Arg Arg Ser Glu
305 310 315

gag atg cca att tcg aat ctc tgt cgt aag agt tcc acc gat gtg gta 1369
Glu Met Pro Ile Ser Asn Leu Cys Arg Lys Ser Ser Thr Asp Val Val
320 325 330 335

aat agt tcc cag agg ccg tct gac ggg cag tgg ggt ctc caa gtg tgt 1417
Asn Ser Ser Gln Arg Pro Ser Asp Gly Gln Trp Gly Leu Gln Val Cys
340 345 350

tgaatgccat gaagacaaat ggcccagcag caaagcagag acctgggcaa ctgtgagtta 1477

aatctgaagg gtgaggggact tgaaaaatga cagccccccc ccccgccca cccgcccgcc 1537

cgccccgctc tttctcagct gtgtctttct cactcaagta gaagcaaaat ctaaaaaaaa 1597

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catgcgacgt c 1668

<210> 6

<211> 351

<212> PRT

<213> Rattus norvegicus

<400> 6

Met Leu Phe Leu Ser Pro Ser Ala Met Asp Asn Gly Ser Cys Cys Leu
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Met Pro Ile Ser Asn Leu Cys Arg Lys Ser Ser Thr Asp Val Val Asn
 325 330 335

Ser Ser Gln Arg Pro Ser Asp Gly Gln Trp Gly Leu Gln Val Cys
 340 345 350

<210> 7
 <211> 15
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 7
 Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1 5 10 15

<210> 8
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: internalizing
 domain derived from HIV tat protein

<400> 8
 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
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<210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 9
 aagaggacca ggcggcaggg aatat 25

<210> 10
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 10
 tatcccccaa aatccaatgc ctacg 25

<210> 11
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: forward primer

<400> 11
cgggcaggtg ggtgatgagg ttag 24

<210> 12
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: reverse primer

<400> 12
gctgctgggc catttgtctt cat 23

<210> 13
<211> 21
<212> DNA
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<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 13
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<210> 14
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 14
gaatagggcc ggaagcattg t 21

<210> 15
<211> 23
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<220>
<223> Description of Artificial Sequence: PCR primer

<400> 15

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23

<210> 16

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 16

cctttgtgtc agccacctag gatgc

25

<210> 17

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 17

ttcacgttgg ccatgaaca

19

<210> 18

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 18

aaatacctgt ccgcagcc

18

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 19

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24

<210> 20

<211> 15

<212> DNA

<213> Artificial Sequence

[illegible]